```
L1
           19214 S NEMATODE OR C.ELEGANS OR ?ELEGANS
L2
              509 S PROLYL ?HYDROXYLASE
L3
                2 S L1 (S) L2
L4
                2 S L1 (L) L2
L5
                 S DPY-18
L6
              103 S DPY-18 OR DPY
L7
               59 S L1 (L) L6
                0 S L7 AND L2
=> FILE CAPLUS MEDLINE BIOSIS EMBASE
                                                        SINCE FILE
                                                                          TOTAL
COST IN U.S. DOLLARS
                                                             ENTRY
                                                                        SESSION
FULL ESTIMATED COST
                                                               3.06
                                                                           3.27
FILE 'CAPLUS' ENTERED AT 14:49:21 ON 18 JUL 2002
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
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FILE 'MEDLINE' ENTERED AT 14:49:21 ON 18 JUL 2002
FILE 'BIOSIS' ENTERED AT 14:49:21 ON 18 JUL 2002
COPYRIGHT (C) 2002 BIOLOGICAL ABSTRACTS INC.(R)
FILE 'EMBASE' ENTERED AT 14:49:21 ON 18 JUL 2002
COPYRIGHT (C) 2002 Elsevier Science B.V. All rights reserved.
=> S L3
L9
             11 L3
=> DUP REM L9
PROCESSING COMPLETED FOR L9
                6 DUP REM L9 (5 DUPLICATES REMOVED)
=> D 1-6 IBIB ABS
L10 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2002 ACS
                                                              DUPLICATE 1
                            2001:757463 CAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                            136:33452
                            C. elegans EGL-9 and mammalian homologs define a
TITLE:
                            family of dioxygenases that regulate HIF by prolyl
                            hydroxylation
                            Epstein, Andrew C. R.; Gleadle, Jonathan M.; McNeill, Luke A.; Hewitson, Kirsty S.; O'Rourke, John; Mole,
AUTHOR(S):
                            David R.; Mukherji, Mridul; Metzen, Eric; Wilson,
                            Michael I.; Dhanda, Anu; Tian, Ya-Min; Masson, Norma;
                            Hamilton, Donald L.; Jaakkola, Panu; Barstead, Robert;
                            Hodgkin, Jonathan; Maxwell, Patrick H.; Pugh, Christopher W.; Schofield, Christopher J.; Ratcliffe,
                            Peter J.
CORPORATE SOURCE:
                            The Henry Wellcome Building of Genomic Medicine,
                            Oxford, OX3 7BN, UK
                            Cell (Cambridge, MA, United States) (2001), 107(1),
SOURCE:
                            43-54
                            CODEN: CELLB5; ISSN: 0092-8674
                            Cell Press
PUBLISHER:
DOCUMENT TYPE:
                            Journal
                            English
LANGUAGE:
     HIF is a transcriptional complex that plays a central role in mammalian
     oxygen homeostasis. Recent studies have defined posttranslational
     modification by prolyl hydroxylation as a key regulatory event that
     targets HIF-.alpha. subunits for proteasomal destruction via the von
     Hippel-Lindau ubiquitylation complex. Here, we define a conserved HIF-VHL- ***prolyl*** ***hydroxylase*** pathway in ***C***
        dioxygenase that regulates HIF by prolyl hydroxylation. In mammalian
     cells, we show that the HIF-prolyl hydroxylases are represented by a
     series of isoforms bearing a conserved 2-histidine-1-carboxylate iron coordination motif at the catalytic site. Direct modulation of recombinant enzyme activity by graded hypoxia, iron chelation, and cobaltous ions mirrors the characteristics of HIF induction in vivo,
     fulfilling requirements for these enzymes being oxygen sensors that
     regulate HIF.
REFERENCE COUNT:
                            40
                                   THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS
                                   RECORD, ALL CITATIONS AVAILABLE IN THE RE FORMAT
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FILE 'MEDLINE' ENTERED AT 14:44:53 ON 18 JUL 2002

ANSWER 2 OF 6 CAPLUS COPYRIGHT 2002 ACS 2000:324546 CAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER:

133:86929

TITLE:

Prolyl 4-hydroxylase is an essential

procollagen-modifying enzyme required for exoskeleton formation and the maintenance of body shape in the

nematode Caenorhabditis elegans

Winter, Alan D.; Page, Antony P. Wellcome Centre for Molecular Parasitology, Anderson AUTHOR(S): CORPORATE SOURCE:

College, The University of Glasgow, Glasgow, G11 6NU,

DUPLICATE 2

SOURCE:

Molecular and Cellular Biology (2000), 20(11),

4084-4093

CODEN: MCEBD4; ISSN: 0270-7306 American Society for Microbiology

**PUBLISHER:** DOCUMENT TYPE: Journal LANGUAGE: English

The multienzyme complex prolyl 4-hydroxylase catalyzes the hydroxylation of proline résidues and acts as a chaperone during collagen synthésis in multicellular organisms. The .beta. subunit of this complex is identical to protein disulfide isomerase (PDI). The free-living nematode C. elegans is encased in a collagenous exoskeleton and represents an excellent model for the study of collagen biosynthesis and extracellular matrix formation. In this study, we examd. prolyl 4-hydroxylase .alpha.-subunit (PHY; EC 1.14.11.2)- and .beta.-subunit (PDI; EC 5.3.4.1)-encoding genes with respect to their role in collagen modification and formation of the C. elegans exoskeleton. We identified genes encoding 2 PHYs and a single assocd. PDI and showed that all 3 are expressed in collagen-synthesizing ectodermal cells at times of maximal collagen synthesis. Disruption of the pdi gene via RNA interference resulted in embryonic lethality. Similarly, the combined phy genes are required for embryonic development. Interference with phy-1 resulted in a morphol. dumpy phenotype, which we detd. to be identical to the uncharacterized dpy-18 locus. Two dpy-18 mutant strains were shown to have null alleles for phy-1 and to have a reduced hydroxyproline content in their exoskeleton collagens. This study demonstrates in vivo that this enzyme complex plays a central role in extracellular matrix formation and is essential for normal metazoan development.

38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS REFERENCE COUNT: RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 3 OF 6 **MEDLINE** 79021663

ACCESSION NUMBER: MEDLINE

PubMed ID: 212107 DOCUMENT NUMBER: 79021663

TITLE: In vitro translation of nematode cuticular collagens.

Noble S; Leushner J; Pasternak J **AUTHOR:** 

BIOCHIMICA ET BIOPHYSICA ACTA, (1978 Aug 23) 520 (1) SOURCE:

219-28.

Journal code: 0217513. ISSN: 0006-3002.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

English LANGUAGE:

Priority Journals FILE SEGMENT:

ENTRY MONTH: 197812

**ENTRY DATE:** Entered STN: 19900314

Last Updated on STN: 19900314

Entered Medline: 19781220

Phenanthroline treatment of growing cultures of the free-living

\*\*\*nematode\*\*\* Panagrellus silusiae was used to lower the degree of hydroxylation of nascent collagen chains at the polysomal level. Under AB these conditions, the bound pentasome-hexasome fraction provided substrate for \*\*\*prolyl\*\*\* \*\*\*hydroxylase\*\*\* . When this polysomal fraction for \*\*\*prolyl\*\*\* \*\*\*hydroxylase\*\*\* . When this polysomal fraction was subsequently tested in a cell-free wheat germ system, collagenase-susceptible translation products were observed after sodium dodecyl sulfate-acrylamide gel electrophoresis. The electrophoretic mobilities of each of these four major collagen products were similar to four collagens that are isolated from intact cuticles. In addition, purified polysomal RNA that adhered to unmodified cellulose directed the synthesis of four pepsin-resistant polypeptides that had molecular weights that coincided with four pepsin-resistant collagens that can be purified from the cuticle of this species. Thus, the polysomal site of the messenger RNAs for the cuticular collagens of P. silusiae was located. Although precursor forms of the cuticular collagens were not produced in the cell-free system, the question whether additional amino acid segments occur on the primary translational products of the cuticular collagens in vivo remains open.

L10 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 3

1978:185080 CAPLUS ACCESSION NUMBER: 88:185080

DOCUMENT NUMBER: Partial purification and characterization of \*\*\*prolyl\*\*\* \*\*\*hydroxylase\*\*\* from TITLE:

free-living \*\*\*nematode\*\*\* Panagrellus silus Leushner, J. R. A.; Pasternak, J. Dep. Biol., Univ. Waterloo, Waterloo, Ont., Can. Can. J. Zool. (1978), 56(2), 159-65 CODEN: CJZOAG; ISSN: 0008-4301 Panagrellus silusiae

AUTHOR(S):

CORPORATE SOURCE:

SOURCE:

DOCUMENT TYPE: Journal LANGUAGE: English

\*\*\*Prolvl\*\*\* \*\*\*hydroxylase\*\*\* (I) was partially purified from the \*\*\*nematode\*\*\* P. silusiae and its physicochem. and biol. properties

were studied. I purifn. involved (NH4)2504 pptn. and Ca phosphate gel ion

exchange from Triton X-100-treated Panagrellus homogenates. Gel filtration indicated a mol. wt. of .apprx.285,000; acrylamide electrophoresis showed the component to be comprised of subunits having mol. wts. of .apprx.67,000. I activity was dependent on

.alpha.-ketoglutarate, Fe2+, ascorbate, catalase, O, and dithiothreitol. Activity was inhibited by .alpha.,.alpha.-dipyridyl, phenanthroline, and polyproline. The Km value for the substrate was 80 .mu.g.

L10 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

1978:67206 BIOSIS ACCESSION NUMBER:

DOCUMENT NUMBER: BR15:10706

\*\*\*PROLYL\*\*\* \*\*\*HYDROXYLASE\*\*\* PROTO COLLAGEN TN TITLE: \*\*\*NEMATODE\*\*\* THE FREE LIVING PANAGRELLUS-SILUSIAE.

LEUSHNER J R A; PASTERNAK J J AUTHOR(S):

**SOURCE:** Proc. Can. Fed. Biol. Soc., (1976) 19, 98.

CODEN: PCBSA2.

DOCUMENT TYPE: Conference FILE SEGMENT: BR; OLD LANGUAGE: Unavailable

EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V. L10 ANSWER 6 OF 6

76171264 EMBASE ACCESSION NUMBER:

DOCUMENT NUMBER: 1976171264

Programmed synthesis of collagen during postembryonic TITLE:

development of the nematode Panagrellus silusiae.

AUTHOR: Leushner J.; Pasternak J.

CORPORATE SOURCE:

Dept. Biol., Univ. Waterloo, Canada Developmental Biology, (1975) 47/1 (68-80). SOURCE:

CODEN: DEBIAO

DOCUMENT TYPE: Journal

Clinical Biochemistry FILE SEGMENT: 029

> 021 Developmental Biology and Teratology

Enalish LANGUAGE:

The relative rate of collagen synthesis in the free living

\*\*\*nematode\*\*\* Panagrellus silusiae during postembryonic development was

found to be discontinuous by measuring either the incorporation of tritium into material extracted as collagen or the amount of collagen bound

tritiated proline and hydroxyproline after 2 hr incubations of whole worms with [3H]proline. A peak of collagen production preceded each of the three

molts that were examined. Moreover, protocollagen \*\*\*prolyl\*\*\*

\*\*\*hydroxylase\*\*\* activity during each intermolt period paralleled the pattern of collagen synthesis. On the other hand, a triphasic pattern was not observed when noncollagenous proteins were labeled with either [3H]tryptophan or [3H]leucine. In addition, the level of soluble radioactive proline that accumulates in whole organisms after 2 hr incubation periods did not fluctuate appreciably during postembryonic development. The mean ratio of hydroxyproline to proline in a number of collagen samples extracted at various times during the maturation phase was 0.113 .+-. 0.040. Pulse and chase experiments with [3H]proline indicated that most of the collagen synthesized during a peak period is lost after the second ecdysis following the labeling interval. In contrast, a considerable proportion of the collagen synthesized during nonpeak periods is retained throughout the postembryonic period. It is postulated that the modulated pattern of collagen biosynthesis in Panagrellus reflects, for the most part, a quantitative regulation of the production of cuticular collagen during postembryonic development.

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L1
           19214 S NEMATODE OR C.ELEGANS OR ?ELEGANS
L2
             509 S PROLYL ?HYDROXYLASE
L3
L4
L5
               2 S L1 (S) L2
               2 S L1 (L) L2
               7 S DPY-18
L6
L7
             103 S DPY-18 OR DPY
              59 S L1 (L) L6
               0 S L7 AND L2
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L9
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L10
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=> S L5
             25 L5
L11
=> S EMBRYONAL LETHAL PHENOTYPE
              O EMBRYONAL LETHAL PHENOTYPE
L12
=> S EMBRYONIC LETHAL PHENOTYPE
            283 EMBRYONIC LETHAL PHENOTYPE
=> S EMBRYON? LETHAL PHENOTYPE
            290 EMBRYON? LETHAL PHENOTYPE
L14
=> S EMBRYON? LETHA? PHENOTYPE
            290 EMBRYON? LETHA? PHENOTYPE
L15
=> S L1 (s) L15
             35 L1 (S) L15
L16
=> S L16 AND L2
              0 L16 AND L2
L17
=> S L1 (s) L15 (s) L2
L18
              0 L1 (S) L15 (S) L2
=> S L1 (L) L15 (L) L2
              0 L1 (L) L15 (L) L2
L19
=> D HIS
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     FILE 'MEDLINE' ENTERED AT 14:44:53 ON 18 JUL 2002
L1
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L2
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               2 S L1 (S) L2
2 S L1 (L) L2
7 S DPY-18
L3
L4
L5
L6
             103 S DPY-18 OR DPY
L7
              59 S L1 (L) L6
               0 S L7 AND L2
L8
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L9
              11 S L3
L10
               6 DUP REM L9 (5 DUPLICATES REMOVED)
              25 S L5
L11
L12
               O S EMBRYONAL LETHAL PHENOTYPE
L13
             283 S EMBRYONIC LETHAL PHENOTYPE
L14
             290 S EMBRYON? LETHAL PHENOTYPE
             290 S EMBRYON? LETHA? PHENOTYPE
L15
L16
              35 S L1 (S) L15
               0 S L16 AND L2
L17
               0 S L1 (S) L15
0 S L1 (L) L15
L18
                                (L) L2
L19
=> DUP REM L16
PROCESSING COMPLETED FOR L16
              12 DUP REM L16 (23 DUPLICATES REMOVED)
L20
=> S L6
            421 L6
L21
\Rightarrow S L21 (s) L1
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FILE 'MEDLINE' ENTERED AT 14:44:53 ON 18 JUL 2002

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=> S L21 AND L22
L23
              222 L21 AND L22
=> S L1 (s) L15 (s) L21
L24
                0 L1 (S) L15 (S) L21
=> S L1 (L) L15 (L) L21
                0 L1 (L) L15 (L) L21
L25
=> S L1 AND L15 AND L21
                1 L1 AND L15 AND L21
L26
=> D
L26
      ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS
      1998:454514 CAPLUS
AN
DN
      129:212270
      Isolation and characterization of lethal mutation near the unc-29 (LG I)
TI
                                         ***elegans***
      region of Caenorhabditis
      Lee, Jinsook; Ahnn, Joohong
Department of Life Science, Kwangju Institute of Science and Technology,
ΑU
CS
      Kwangju, 506-712, S. Korea
Korean Journal of Biological Sciences (1998), 2(1), 123-131
SO
      CODEN: KJBSFZ; ISSN: 1226-5071
      Korean Association of Biological Sciences
PB
DT
      Journal
      English
LA
=> D IBIB ABS
L26 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS
                                1998:454514 CAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                                129:212270
                                Isolation and characterization of lethal mutation near
TITLE:
                                the unc-29 (LG I) region of Caenorhabditis
                                   ***elegans***
                                Lee, Jinsook; Ahnn, Joohong
Department of Life Science, Kwangju Institute of
AUTHOR(S):
CORPORATE SOURCE:
                                Science and Technology, Kwangju, 506-712, S. Korea
SOURCE:
                                Korean Journal of Biological Sciences (1998), 2(1),
                                123-131
                                CODEN: KJBSFZ; ISSN: 1226-5071
                                Korean Association of Biological Sciences
PUBLISHER:
DOCUMENT TYPE:
                                Journal
LANGUAGE:
                                English
                                                                                  ***elegans***
      The unc-29 region on the chromosome I of Caenorhabditis
      has been mutagenized in order to obtain lethal mutations. In this screen, the uncoordinated phenotype of unc-29 (e193) mutant was used to identify any lethal mutations closely linked to the unc-29 gene, which encodes a subunit of nicotinic acetylcholine receptors. The authors have isolated six independent mutations (jh1 to jh6) out of approx. 5,200 Et
      methanesulfonate (EMS) treated haploids. Four of the six mutations
                         ***embryonic***
                                                   ***lethal***
                                                                         ***phenotypes***
      demonstrated
      while the other two showed embryonic and larval lethal phenotypes.
Terminal phenotypes obsd. in two mutations (jh1 and jh2) indicated developmental defects specific to posterior part of embryos which appeared similar to the phenotypes obsd. in nob (no back end) mutants. Another
      mutation (jh4) resulted in an interesting phenotype of body-wall muscle
      degeneration at larval stage. These mutations were mapped by using
      three-factor crosses and deficiency mutants in this region. Here the
      authors report genetic anal. and characterization of these lethal
      mutations.
=> D HIS
      (FILE 'HOME' ENTERED AT 14:44:43 ON 18 JUL 2002)
      FILE 'MEDLINE' ENTERED AT 14:44:53 ON 18 JUL 2002
             19214 S NEMATODE OR C.ELEGANS OR ?ELEGANS
L1
L2
               509 S PROLYL ?HYDROXYLASE
L3
                  2 S L1 (S) L2
                  2 S L1 (L) L2
L5
                  7 S DPY-18
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FILE 'CAPLUS, MEDLINE, BIOSIS, EMBASE' ENTERED AT 14:49:21 ON 18 JUL 2002
19
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                  6 DUP REM L9 (5 DUPLICATES REMOVED)
L10
                 25 S L5
L11
                  0 S EMBRYONAL LETHAL PHENOTYPE
L12
L13
               283 S EMBRYONIC LETHAL PHENOTYPE
L14
                290 S EMBRYON? LETHAL PHENOTYPE
               290 S EMBRYON? LETHA? PHENOTYPE
L15
L16
                35 S L1 (S) L15
                 0 S L16 AND L2
0 S L1 (S) L15
0 S L1 (L) L15
L17
                                      (S) L2
(L) L2
L18
L19
                12 DUP RÈM L16 (23 DUPLICATES REMOVED)
L20
L21
               421 S L6
L22
               222 S L21 (S) L1
L23
               222 S L21 AND L22
L24
                 0 S L1 (S) L15 (S) L21 0 S L1 (L) L15 (L) L21
L25
L26
                  1 S L1 AND L15 AND L21
=> DUP REM L22
PROCESSING COMPLETED FOR L22
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L27
=> S L1 AND L11
L28
               21 L1 AND L11
=> S L27 AND L28
                8 L27 AND L28
=> DUP REM L29
PROCESSING COMPLETED FOR L29
                  8 DUP REM L29 (0 DUPLICATES REMOVED)
=> D 1-8 IBIB ABS
L30 ANSWER 1 OF 8
                             MEDLINE
                         2002354365
                                            IN-PROCESS
ACCESSION NUMBER:
                                       PubMed ID: 12097347
DOCUMENT NUMBER:
                         22092148
TITLE:
                         High-Throughput Gene Mapping in Caenorhabditis
                             **elegans***
AUTHOR:
                         Swan Kathryn A; Curtis Damian E; McKusick Kathleen B;
                         Voinov Alexander V; Mapa Felipa A; Cancilla Michael R
CORPORATE SOURCE:
                         Exelixis, Inc., South San Francisco, California 94083-0511,
                         USA.
                         GENOME RESEARCH, (2002 Jul) 12 (7) 1100-5.
SOURCE:
                         Journal code: 9518021. ISSN: 1088-9051.
                         United States
PUB. COUNTRY:
                         Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:
                         English
                         IN-PROCESS; NONINDEXED; Priority Journals
FILE SEGMENT:
ENTRY DATE:
                         Entered STN: 20020707
      Last Updated on STN: 20020707
Positional cloning of mutations in model genetic systems is a powerful method for the identification of targets of medical and agricultural
      importance. To facilitate the high-throughput mapping of mutations in Caenorhabditis ***elegans*** , we have identified a further 9602
      putative new single nucleotide polymorphisms (SNPs) between two
           ***elegans***
                               strains, Bristol N2 and the Hawaiian mapping strain
      CB4856, by sequencing inserts from a CB4856 genomic DNA library and using an informatics pipeline to compare sequences with the canonical N2 genomic sequence. When combined with data from other laboratories, our marker set
      of 17,189 SNPs provides even coverage of the complete worm genome. To
      date, we have confirmed >1099 evenly spaced SNPs (one every 91 \pm - 56 kb) across the six chromosomes and validated the utility of our SNP marker set
      and new fluorescence polarization-based genotyping methods for systematic
      and high-throughput identification of genes in
                                                                     ***C***
      ***elegans*** by cloning several proprietary genes. We illustrate our approach by recombination mapping and confirmation of the mutation in the cloned gene, ***dpy*** - ***18*** . [The sequence data described in
      this paper have been submitted to the NCBI dbSNP data library under
      accession nos. 4388625-4389689 and GenBank dbSTS under accession nos
      973810-974874. The following individuals and institutions kindly provided
```

59 S L1 (L) L6

0 S L7 AND L2

L7 L8

\*\*\*/\*\* \*\*\*elegans\*\*\* The Sequencing Consortium and The Caenorhabditis Genetics Center.]

BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC. L30 ANSWER 2 OF 8

ACCESSION NUMBER: 2002:141383 BIOSIS DOCUMENT NUMBER: PREV200200141383

The T-box factor MLS-1 acts as a molecular switch during TITLE:

specification of nonstriated muscle in

\*\*\*elegans\*\*\*

AUTHOR(S): Kostas, Stephen A.; Fire, Andrew (1)

(1) Department of Embryology, Carnegie Institution of CORPORATE SOURCE: Washington, Baltimore, MD, 21210: fire@ciwemb.edu USA

SOURCE:

Genes & Development, (January 15, 2002) Vol. 16, No. 2, pp.

257-269. http://www.genesdev.org/. print.

ISSN: 0890-9369.

Article DOCUMENT TYPE: English LANGUAGE:

We have isolated mutations in a gene mls-1 that is required for proper

specification of nonstriated muscle fates in Caenorhabditis

\*\*\*elegans\*\*\* . Loss of MLS-1 activity causes uterine muscle precursors to forego their normal fates, instead differentiating as vulval muscles. we have cloned mls-1 and shown that the product is a member of the T-box family of transcriptional regulators. MLS-1 acts as a cell fate determinant in that ectopic expression can transform other cell types to uterine muscle precursors. Uterine muscle patterning is executed by regulation of MLS-1 at several different levels. The mls-1 promoter is \*\*\*C\*\*\* . \*\*\*elegans\*\*\* activated by the orthologs of Twist and Daughterless, but is only active in a subset of the lineage where these two transcription factors are present. mls-1 activity also appears to be regulated by posttranscriptional processes, as expression occurs in both uterine and vulval muscle precursors.

L30 ANSWER 3 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

2002:68425 BIOSIS ACCESSION NUMBER: DOCUMENT NUMBER: PREV200200068425

\*\*\*C\*\*\* TITLE: Role of \*\*\*elegans\*\*\* lin-40 MTA in vulval

fate specification and morphogenesis.

AUTHOR(S): Chen, Zhe; Han, Min (1)

(1) Department of Molecular, Cellular and Developmental CORPORATE SOURCE:

Biology, Howard Hughes Medical Institute, University of Colorado at Boulder, Boulder, CO, 80309: mhan@colorado.edu

USA

SOURCE: Development (Cambridge), (December, 2001) Vol. 128, No. 23,

pp. 4911-4921. http://dev.biologists.org/current.shtml.

print.

ISSN: 0950-1991.

DOCUMENT TYPE: Article English LANGUAGE:

Vulval\_differentiation\_in\_Caenorhabditis\_ involves \*\*\*elegans\*\*\* several fundamental cellular events, including cell fusion, division and migration. We have characterized the role of the lin-40 (also known as egr-1) gene in these cellular processes. LIN-40 is homologous to the metastasis-associated factor 1 (MTA1) in mammals, which has been identified as a component of the nucleosome remodeling and histone deacetylation (NuRD) complex that functions as a transcriptional co-repressor. We show here that lin-40 negatively regulates vulval fate specification at least partly by promoting cell fusion between the vulval precursor cells and the hypodermal syncytium at an early larval stage. This inhibitory function of lin-40 might be carried out by downregulating lin-39 Hox expression. We also show that lin-40 is specifically required for cell divisions along the transverse orientation during vulval morphogenesis.

L30 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2002 ACS 2000:296070 CAPLUS ACCESSION NUMBER:

133:233493 DOCUMENT NUMBER:

AUTHOR(S):

CORPORATE SOURCE:

Prolyl 4-hydroxylase is required for viability and TITLE:

morphogenesis in Caenorhabditis \*\*\*elegans\*\*\* Friedman, Lisa; Higgin, Joshua J.; Moulder, Gary; Barstead, Robert; Raines, Ronald T.; Kimble, Judith

Department of Biochemistry, University of Wisconsin, Madison, WI, 53706, USA

Proceedings of the National Academy of Sciences of the SOURCE:

United States of America (2000), 97(9), 4736-4741

CODEN: PNASA6; ISSN: 0027-8424

**PUBLISHER:** National Academy of Sciences

```
The genome of Caenorhabditis
                                                 ***elegans***
AB
                                                                       possesses two genes,
         ***dpy*** - ***18*** and phy-2, that encode .alpha. subunits of the
       enzyme prolyl 4-hydroxylase. Th authors have generated deletions within
       each gene to eliminate prolyl 4-hydroxylase activity from the animal. The ***dpy*** - ***18*** mutant has an aberrant body morphol., consistent
      with a role of prolyl 4-hydroxylase in formation of the body cuticle. The phy-2 mutant is phenotypically wild type. However, the ***dpy*** - ***18***; phy-2 double mutant is not viable, suggesting an essential role for prolyl 4-hydroxylase that is normally accomplished by either ***dpy*** - ***18*** or phy-2. The effects of the double mutation were mimicked by small-mol. inhibitors of prolyl 4-hydroxylase, validating the genetic results and suggesting that ***C*** . ***elegans*** can
       serve as a model system for the discovery of new inhibitors.
                                  50
                                          THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS
REFERENCE COUNT:
                                          RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L30 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER:
                                  2000:324546 CAPLUS
DOCUMENT NUMBER:
                                  133:86929
                                  Prolyl 4-hydroxylase is an essential
TITLE:
                                  procollagen-modifying enzyme required for exoskeleton formation and the maintenance of body shape in the
                                                                                   ***elegans***
                                     ***nematode***
                                                            Caenorhabditis
                                  Winter, Alan D.; Page, Antony P.
Wellcome Centre for Molecular Parasitology, Anderson
AUTHOR(S):
CORPORATE SOURCE:
                                  College, The University of Glasgow, Glasgow, G11 6NU,
                                  Molecular and Cellular Biology (2000), 20(11),
SOURCE:
                                  4084-4093
                                  CODEN: MCEBD4; ISSN: 0270-7306
PUBLISHER:
                                  American Society for Microbiology
DOCUMENT TYPE:
                                  Journal
LANGUAGE:
                                  English
      The multienzyme complex prolyl 4-hydroxylase catalyzes the hydroxylation
      of proline residues and acts as a chaperone during collagen synthesis in
      multicellular organisms. The .beta. subunit of this complex is identical to protein disulfide isomerase (PDI). The free-living ***nematode***

***C*** . ***elegans*** is encased in a collagenous exoskeleton and
       represents an excellent model for the study of collagen biosynthesis and
      extracellular matrix formation. In this study, we examd. prolyl 4-hydroxylase .alpha.-subunit (PHY; EC 1.14.11.2)- and .beta.-subunit
      (PDI; EC 5.3.4.1)-encoding genes with respect to their role in collagen modification and formation of the ***C*** . ***elegans***
      exoskeleton. We identified genes encoding 2 PHYs and a single assocd. PDI
      and showed that all 3 are expressed in collagen-synthesizing ectodermal cells at times of maximal collagen synthesis. Disruption of the pdi gene
      via RNA interference resulted in embryonic lethality. Similarly, the
      combined phy genes are required for embryonic development. Interference
      with phy-1 resulted in a morphol. dumpy phenotype, which we detd. to be identical to the uncharacterized ***dpy*** - ***18*** locus. Two ***dpy*** - ***18*** mutant strains were shown to have null allele
         ***dpy***
                                           mutant strains were shown to have null alleles
       for phy-1 and to have a reduced hydroxyproline content in their
       exoskeleton collagens. This study demonstrates in vivo that this enzyme
       complex plays a central role in extracellular matrix formation and is
      essential for normal metazoan development.
                                          THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS
REFERENCE COUNT:
                                  38
                                          RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L30 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2002 ACS
                                  2000:550782 CAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                                  134:247771
                                                   - ***18***
                                                                     encodes an .alpha.-subunit
                                     ***dpy***
TITLE:
                                  of prolyl-4-hydroxylase in Caenorhabditis
                                    ***elegans***
                                  Hill, Katherine L.; Harfe, Brian D.; Dobbins, Carey
AUTHOR(S):
                                  A.; L'Hernault, Steven W.
                                  Program in Genetics and Molecular Biology, Graduate
CORPORATE SOURCE:
                                  Division of Biological and Biomedical Sciences, Emory
                                  University, Atlanta, GA, 30322, USA
Genetics (2000), 155(3), 1139-1148
SOURCE:
                                  CODEN: GENTAE; ISSN: 0016-6731
PUBLISHER:
                                  Genetics Society of America
DOCUMENT TYPE:
                                  Journal
LANGUAGE:
                                  English
      Collagen is an extracellular matrix (ECM) component encoded by a large
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LANGUAGE:

English

post-translationally modified by prolyl-4-hydroxylase (EC 1.14.11.2) before secretion and participation in ECM formation. Therefore, collagen processing and regulation can be studied by examg. this required interaction of prolyl-4-hydroxylase with procollagen. High-resoln.

nolymorphism manning was used to place the Caenorhabditis \*\*\*elegans\*\*\* polymorphism mapping was used to place the Caenorhabditis \*\*\*elegans\*\*\*

\*\*\*dpy\*\*\* - \*\*\*18\*\*\* gene on the phys. map, and we show that it
encodes a prolyl-4-hydroxylase .alpha. catalytic subunit. The Dpy
phenotype of \*\*\*dpy\*\*\* - \*\*\*18\*\*\* (e364) amber mutants is more severe
when this mutation is in trans to the noncomplementing deficiency tDf7,
while the \*\*\*dpy\*\*\* - \*\*\*18\*\*\* (e499) deletion mutant exhibits the
same phenotype as \*\*\*dpy\*\*\* - \*\*\*18\*\*\* (e499)/tDf7. Furthermore,

\*\*\*dpy\*\*\* - \*\*\*18\*\*\* RNA interference (RNAi) in wild-type worms \*\*\*dpy\*\*\* - \*\*\*18\*\*\* RNA interference (RNAi) in wild-type worms results in Dpy progeny, while \*\*\*dpy\*\*\* - \*\*\*18\*\*\* (RNAi) in \*\*\*dpy\*\*\* - \*\*\*18\*\*\* (e499) mutants does not alter the Dpy phenotype of their progeny. These observations suggest that the \*\*\*dpy\*\*\* - \*\*\*18\*\*\* null phenotype is Dpy. A \*\*\*dpy\*\*\* - \*\*\*18\*\*\* ::gfp promoter fusion construct is expressed throughout the hypodermis within the cells that abundantly produce the cuticle collagens, as well as in certain head and posterior neurons. While prolyl-4-hydroxylase has been studied extensively by biochem, techniques, this is the first report of a mutationally definéd prolyl-4-hydroxylase in any animal. RENCE COUNT: 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS REFERENCE COUNT: RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC. 2000:323602 BIOSIS ACCESSION NUMBER: PREV200000323602 Mutations with sensory ray defect unmask cuticular glycoprotein antigens in Caenorhabditis \*\*\*elegans\*\*\* TITLE: male tail Ko, Frankie C. F.; Chow, King L. (1)
(1) Department of Biology, Hong Kong University of Science AUTHOR(S):CORPORATE SOURCE: and Technology, Clear Water Bay, Kowloon, Hong Kong China Development Growth & Differentiation, (Feb., 2000) Vol. 42, SOURCE:

L30 ANSWER 7 OF 8

DOCUMENT NUMBER:

No. 1, pp. 69-77. print. ISSN: 0012-1592.

DOCUMENT TYPE: Article English LANGUAGE: English SUMMARY LANGUAGE:

\*\*\*elegans\*\*\* Caenorhabditis male tail has nine pairs of bilaterally symmetric ray processes extended into a cuticular fan. The formation of these structures involves both cell lineage differentiation and cellular morphogenesis. Nine mutations were examined, all of which presented an amorphous ray phenotype. Glycoconjugates carrying an N-acetylglucosamine (GlcNAc) epitope were detected at a high level in their male bursa. It was shown that these antigens are not responsible for the morphological defects. It was further demonstrated that these ram and mab gene products represent critical components for male tail cuticle organization. Mutations of them abolish the integrity of the male bursal cuticle and unmask the underlying GlcNAc epitope.

L30 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2002 ACS 1991:116067 CAPLUS ACCESSION NUMBER:

114:116067 DOCUMENT NUMBER:

Properties of a class of genes required for ray TITLE: \*\*\*elegans\*\*\* morphogenesis in Caenorhabditis

Baird, Scott E.; Emmons, Scott W.

AUTHOR(S): Dep. Mol. Genet., Albert Einstein Coll. Med., Bronx, NY, 10461, USA CORPORATE SOURCE:

Genetics (1990), 126(2), 335-44 SOURCE:

CODEN: GENTAE; ISSN: 0016-6731

DOCUMENT TYPE: Journal LANGUAGE: English

Eight mutations were identified in Caenorhabditis \*\*\*elegans\*\*\* define at least 5 terminal differentiation genes (ram genes) whose products are required during the extension of the male-specific ray sensilla. ram Gene mutations result in morphol. abnormalities in the sensory rays but do not appear to interfere with ray functions. A similar ray morphol. phenotype was obsd. in males harboring mutations in 3 previously defined genes, dpy-11, \*\*\*dpy\*\*\* - \*\*\*18\*\*\*, and sqt-1, that also affect body shape. One of these genes, sqt-1, is known to encode a collagen. Mutations in different ram genes failed to complement, suggesting that their gene products functionally interact. For one ram gene, failure to complement was shown to result from haploinsufficiency. Intergenic noncomplementation did not extend to the body morphol. genes. The temp.-sensitive periods of both ram and body morphol. mutations

It is proposed that ram gene products act together in a crit. interaction between the rays and the cuticle required for wild-type ray morphol.

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L4
               2 S L1 (L) L2
                 S DPY-18
L5
L6
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L7
              59 S L1 (L) L6
               0 S L7 AND L2
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L15
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L26
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              21 S L1 AND L11
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               8 S L27 AND L28
               8 DUP REM L29 (0 DUPLICATES REMOVED)
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photomorphogenesis and dwarfism (cpd) mutant. Measurements of endogenous brassinosteroid levels by gas chromatog.-mass spectrometry were consistent with this hypothesis. To examine brassinosteroid-regulated gene expression in dpy, we performed cDNA subtractive hybridization and isolated a novel xyloglucan endotransglycosylase that is regulated by brassinosteroid treatment. The curl-3 (cu-3) mutant (Lycopersicon pimpinellifolium [Jusl.] Mill.) shows extreme dwarfism, altered leaf morphol., de-etiolation, and reduced fertility, all strikingly similar to the Arabidopsis mutant brassinosteroid insensitive 1 (bri1). Primary root elongation of wild-type L. pimpinellifolium seedlings was strongly inhibited by brassinosteroid application, while cu-3 mutant roots were able to elongate at the same brassinosteroid concn. Moreover, cu-3 mutants retained sensitivity to indole-3-acetic acid, cytokinins, gibberellin, and abscisic acid while showing hypersensitivity to 2,4-dichlorophenoxyacetic acid in the root elongation assay. The cu-3 root response to hormones, coupled with its bril-like phenotype, suggests that cu-3 may also be brassinosteroid insensitive.

REFERENCE COUNT:

57

THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L33 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2002 ACS

DUPLICATE 3

ACCESSION NUMBER: 1994:209702 CAPLUS

DOCUMENT NUMBER:

120:209702

TITLE:

Molecular and genetic analyses of the Caenorhabditis elegans dpy-2 and dpy-10 collagen genes: A variety of molecular alterations affect organismal morphology

AUTHOR(S):

Levy, Adam D.; Yang, Jie; Kramer, James M. Med. Sch., Northwestern Univ., Chicago, IL, 60611, USA Mol. Biol. Cell (1993), 4(8), 803-17

CORPORATE SOURCE:

SOURCE:

CODEN: MBCEEV; ISSN: 1059-1524

Journal English

result in severe morphol. changes in C. elegans.

DOCUMENT TYPE: LANGUAGE:

> The authors have identified and cloned the Caenorhabditis elegans dpy-2 and dpy-10 genes and detd. that they encode collagens. Genetic data suggested that these genes are important in morphogenesis and possibly other developmental events. These data include the morphol. phenotypes exhibited by mutants, unusual genetic interactions with the sqt-1 collagen gene, and suppression of mutations in the glp-1 and mup-1 genes. The proximity of the dpy-2 and dpy-10 genes (3.5 kilobase) and the structural similarity of their encoded proteins (41% amino acid identity) indicate that dpy-2 and dpy-10 are the result of a gene duplication event. The genes do not, however, appear to be functionally redundant, because a dpy-10 null mutant is not rescued by the dpy-2 gene. In addn., full complementation between dpy-2 and dpy-10 can be demonstrated with all recessive alleles tested in trans. Sequence anal. of several mutant alleles of each gene was performed to det. the nature of the mol. defects that can cause the morphol. phenotypes. Glycine substitutions within the Gly-X-Y portion of the collagens can result in dumpy (Dpy), dumpy, left roller (DLRol), or temp.-sensitive DLRol phenotypes. Dpy-10(cn64), a dominant temp.-sensitive DLRol allele, creates an Arg-to-Cys substitution in the amino non-Gly-X-Y portion of the protein. Three dpy-10 alleles contain Tcl insertions in the coding region of the gene. Dpy-10(cg36) (DLRol) creates a nonsense codon near the end of the Gly-X-Y region. The nature of this mutation, combined with genetic data, indicates that DLRol is the null phenotype of dpy-10. The Dpy phenotype results from reduced function of the dpy-10 collagen gene. The authors' results indicate that a variety of mol. defects in these collagens can

the genetic results and suggesting that C. elegans can

serve as a model system for the discovery of new inhibitors.

REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2002 ACS ACCESSION NUMBER: 2000:324546 CAPLUS

DOCUMENT NUMBER: 133:86929

AUTHOR (S):

PUBLISHER:

TITLE: Prolyl 4-hydroxylase is an essential

procollagen-modifying enzyme required for exoskeleton formation and the maintenance of body shape in the

nematode Caenorhabditis elegans
Winter, Alan D.; Page, Antony P.

CORPORATE SOURCE: Wellcome Centre for Molecular Parasitology, Anderson

College, The University of Glasgow, Glasgow, G11 6NU,

UK

SOURCE: Molecular and Cellular Biology (2000), 20(11),

4084-4093

CODEN: MCEBD4; ISSN: 0270-7306 American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

AB The multienzyme complex prolyl 4-hydroxylase catalyzes the hydroxylation of proline residues and acts as a chaperone during collagen synthesis in multicellular organisms. The .beta. subunit of this complex is identical

to protein disulfide isomerase (PDI). The free-living nematode

C. elegans is encased in a collagenous exoskeleton and represents an excellent model for the study of collagen biosynthesis and extracellular matrix formation. In this study, we examd. prolyl 4-hydroxylase .alpha.-subunit (PHY; EC 1.14.11.2) - and .beta.-subunit (PDI; EC 5.3.4.1) -encoding genes with respect to their role in collagen modification and formation of the C. elegans

exoskeleton. We identified genes encoding 2 PHYs and a single assocd. PDI and showed that all 3 are expressed in collagen-synthesizing ectodermal cells at times of maximal collagen synthesis. Disruption of the pdi gene via RNA interference resulted in embryonic lethality. Similarly, the combined phy genes are required for embryonic development. Interference with phy-1 resulted in a morphol. dumpy phenotype, which we detd. to be identical to the uncharacterized dpy-18 locus. Two

dpy-18 mutant strains were shown to have null alleles

for phy-1 and to have a reduced hydroxyproline content in their exoskeleton collagens. This study demonstrates in vivo that this enzyme complex plays a central role in extracellular matrix formation and is essential for normal metazoan development.

REFERENCE COUNT: 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2002 ACS ACCESSION NUMBER: 2000:550782 CAPLUS

DOCUMENT NUMBER: 134:247771

TITLE: dpy-18 encodes an .alpha.-subunit

of prolyl-4-hydroxylase in Caenorhabditis

elegans

AUTHOR(S): Hill, Katherine L.; Harfe, Brian D.; Dobbins, Carey

A.; L'Hernault, Steven W.

CORPORATE SOURCE: Program in Genetics and Molecular Biology, Graduate

Division of Biological and Biomedical Sciences, Emory

University, Atlanta, GA, 30322, USA

Genetics (2000), 155(3), 1139-1148 CODEN: GENTAE; ISSN: 0016-6731

PUBLISHER: Genetics Society of America

DOCUMENT TYPE: Journal LANGUAGE: English

SOURCE:

AB Collagen is an extracellular matrix (ECM) component encoded by a large

multigene family in multicellular animals. Procollagen is post-translationally modified by prolyl-4-hydroxylase (EC 1.14.11.2) before secretion and participation in ECM formation. Therefore, collagen processing and regulation can be studied by examg. this required interaction of prolyl-4-hydroxylase with procollagen. High-resoln. polymorphism mapping was used to place the Caenorhabditis elegans dpy-18 gene on the phys. map, and we show that it encodes a prolyl-4-hydroxylase .alpha. catalytic subunit. The Dpy phenotype of dpy-18(e364) amber mutants is more severe when this mutation is in trans to the noncomplementing deficiency tDf7, while the dpy-18(e499) deletion mutant exhibits the same phenotype as dpy-18(e499)/tDf7. Furthermore, dpy-18 RNA interference (RNAi) in wild-type worms results in Dpy progeny, while dpy-18 (RNAi) in dpy-18 (e499) mutants does not alter the Dpy phenotype of their progeny. These observations suggest that the dpy-18 null phenotype is Dpy. A dpy-18::gfp promoter fusion construct is expressed throughout the hypodermis within the cells that abundantly produce the cuticle collagens, as well as in certain head and posterior neurons. While prolyl-4-hydroxylase has been studied extensively by biochem. techniques, this is the first report of a

mutationally defined prolyl-4-hydroxylase in any animal.

REFERENCE COUNT: 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L30 ANSWER 7 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2000:323602 BIOSIS DOCUMENT NUMBER: PREV200000323602

DOCUMENT NUMBER: PREV20000323602

TITLE: Mutations with sensory ray defect unmask cuticular glycoprotein antigens in Caenorhabditis **elegans** 

male tail.

AUTHOR(S): Ko, Frankie C. F.; Chow, King L. (1)

CORPORATE SOURCE: (1) Department of Biology, Hong Kong University of Science

and Technology, Clear Water Bay, Kowloon, Hong Kong China Development Growth & Differentiation, (Feb., 2000) Vol. 42,

No. 1, pp. 69-77. print.

ISSN: 0012-1592.

DOCUMENT TYPE: Article LANGUAGE: English SUMMARY LANGUAGE: English

SOURCE:

Caenorhabditis elegans male tail has nine pairs of bilaterally symmetric ray processes extended into a cuticular fan. The formation of these structures involves both cell lineage differentiation and cellular morphogenesis. Nine mutations were examined, all of which presented an amorphous ray phenotype. Glycoconjugates carrying an N-acetylglucosamine (GlcNAc) epitope were detected at a high level in their male bursa. It was shown that these antigens are not responsible for the morphological defects. It was further demonstrated that these ram and mab gene products represent critical components for male tail cuticle organization. Mutations of them abolish the integrity of the male bursal cuticle and unmask the underlying GlcNAc epitope.

L30 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2002 ACS ACCESSION NUMBER: 1991:116067 CAPLUS

DOCUMENT NUMBER: 114:116067

TITLE: Properties of a class of genes required for ray

morphogenesis in Caenorhabditis elegans

AUTHOR(S): Baird, Scott E.; Emmons, Scott W.

CORPORATE SOURCE: Dep. Mol. Genet., Albert Einstein Coll. Med., Bronx,

NY, 10461, USA

SOURCE: Genetics (1990), 126(2), 335-44

CODEN: GENTAE; ISSN: 0016-6731

DOCUMENT TYPE: Journal LANGUAGE: English

Eight mutations were identified in Caenorhabditis elegans that ΑB define at least 5 terminal differentiation genes (ram genes) whose products are required during the extension of the male-specific ray sensilla. ram Gene mutations result in morphol. abnormalities in the sensory rays but do not appear to interfere with ray functions. A similar ray morphol. phenotype was obsd. in males harboring mutations in 3 previously defined genes, dpy-11, dpy-18, and sqt-1, that also affect body shape. One of these genes, sqt-1, is known to encode a collagen. Mutations in different ram genes failed to complement, suggesting that their gene products functionally interact. For one ram gene, failure to complement was shown to result from haploinsufficiency. Intergenic noncomplementation did not extend to the body morphol. genes. The temp.-sensitive periods of both ram and body morphol. mutations corresponded to the period of development in which ray extension occurs. It is proposed that ram gene products act together in a crit. interaction between the rays and the cuticle required for wild-type ray morphol.

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L3
             2 S L1 (S) L2
L4
             2 S L1 (L) L2
             7 S DPY-18
L5
L6
           103 S DPY-18 OR DPY
L7
            59 S L1 (L) L6
L8
             0 S L7 AND L2
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             0 S EMBRYONAL LETHAL PHENOTYPE
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L26 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1998:454514 CAPLUS

DOCUMENT NUMBER: 129:212270

TITLE: Isolation and characterization of lethal mutation near

the unc-29 (LG I) region of Caenorhabditis

elegans

AUTHOR(S): Lee, Jinsook; Ahnn, Joohong

CORPORATE SOURCE: Department of Life Science, Kwangju Institute of

Science and Technology, Kwangju, 506-712, S. Korea Korean Journal of Biological Sciences (1998), 2(1),

123-131

CODEN: KJBSFZ; ISSN: 1226-5071

PUBLISHER: Korean Association of Biological Sciences

DOCUMENT TYPE: Journal LANGUAGE: English

SOURCE:

The unc-29 region on the chromosome I of Caenorhabditis elegans AΒ has been mutagenized in order to obtain lethal mutations. In this screen, the uncoordinated phenotype of unc-29 (e193) mutant was used to identify any lethal mutations closely linked to the unc-29 gene, which encodes a subunit of nicotinic acetylcholine receptors. The authors have isolated six independent mutations (jh1 to jh6) out of approx. 5,200 Et methanesulfonate (EMS) treated haploids. Four of the six mutations demonstrated embryonic lethal phenotypes, while the other two showed embryonic and larval lethal phenotypes. Terminal phenotypes obsd. in two mutations (jh1 and jh2) indicated developmental defects specific to posterior part of embryos which appeared similar to the phenotypes obsd. in nob (no back end) mutants. Another mutation (jh4) resulted in an interesting phenotype of body-wall muscle degeneration at larval stage. These mutations were mapped by using three-factor crosses and deficiency mutants in this region. Here the authors report genetic anal. and characterization of these lethal mutations.

regulation of MLS-1 at several different levels. The mls-1 promoter is activated by the **C**. **elegans** orthologs of Twist and Daughterless, but is only active in a subset of the lineage where these two transcription factors are present. mls-1 activity also appears to be regulated by posttranscriptional processes, as expression occurs in both uterine and vulval muscle precursors.

L30 ANSWER 3 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:68425 BIOSIS DOCUMENT NUMBER: PREV200200068425

TITLE: Role of **C. elegans** lin-40 MTA in vulval fate specification and morphogenesis.

AUTHOR(S): Chen, Zhe; Han, Min (1)

CORPORATE SOURCE: (1) Department of Molecular, Cellular and Developmental

Biology, Howard Hughes Medical Institute, University of Colorado at Boulder, Boulder, CO, 80309: mhan@colorado.edu

USA

SOURCE: Development (Cambridge), (December, 2001) Vol. 128, No. 23,

pp. 4911-4921. http://dev.biologists.org/current.shtml.

print.

ISSN: 0950-1991.

DOCUMENT TYPE: Article LANGUAGE: English

Vulval differentiation in Caenorhabditis elegans involves several fundamental cellular events, including cell fusion, division and migration. We have characterized the role of the lin-40 (also known as egr-1) gene in these cellular processes. LIN-40 is homologous to the metastasis-associated factor 1 (MTA1) in mammals, which has been identified as a component of the nucleosome remodeling and histone deacetylation (NuRD) complex that functions as a transcriptional co-repressor. We show here that lin-40 negatively regulates vulval fate specification at least partly by promoting cell fusion between the vulval precursor cells and the hypodermal syncytium at an early larval stage. This inhibitory function of lin-40 might be carried out by downregulating lin-39 Hox expression. We also show that lin-40 is specifically required for cell divisions along the transverse orientation during vulval morphogenesis.

L30 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2002 ACS ACCESSION NUMBER: 2000:296070 CAPLUS

DOCUMENT NUMBER: 133:233493

TITLE: Prolyl 4-hydroxylase is required for viability and

morphogenesis in Caenorhabditis elegans

AUTHOR(S): Friedman, Lisa; Higgin, Joshua J.; Moulder, Gary; Barstead, Robert; Raines, Ronald T.; Kimble, Judith

CORPORATE SOURCE: Department of Biochemistry, University of Wisconsin,

Madison, WI, 53706, USA

SOURCE: Proceedings of the National Academy of Sciences of the

United States of America (2000), 97(9), 4736-4741

CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal LANGUAGE: English

AB The genome of Caenorhabditis **elegans** possesses two genes,

dpy-18 and phy-2, that encode .alpha. subunits of the
enzyme prolyl 4-hydroxylase. Th authors have generated deletions within
each gene to eliminate prolyl 4-hydroxylase activity from the animal. The
dpy-18 mutant has an aberrant body morphol., consistent
with a role of prolyl 4-hydroxylase in formation of the body cuticle. The
phy-2 mutant is phenotypically wild type. However, the dpy-

18; phy-2 double mutant is not viable, suggesting an essential role for prolyl 4-hydroxylase that is normally accomplished by either

dpy-18 or phy-2. The effects of the double mutation

were mimicked by small-mol. inhibitors of prolyl 4-hydroxylase, validating

L30 ANSWER 1 OF 8 MEDLINE

ACCESSION NUMBER: 2002354365 IN-PROCESS

DOCUMENT NUMBER: 22092148 PubMed ID: 12097347

TITLE: High-Throughput Gene Mapping in Caenorhabditis

elegans.

AUTHOR: Swan Kathryn A; Curtis Damian E; McKusick Kathleen B;

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CORPORATE SOURCE: Exelixis, Inc., South San Francisco, California 94083-0511,

USA.

SOURCE: GENOME RESEARCH, (2002 Jul) 12 (7) 1100-5.

Journal code: 9518021. ISSN: 1088-9051.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals

ENTRY DATE: Entered STN: 20020707

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AB Positional cloning of mutations in model genetic systems is a powerful method for the identification of targets of medical and agricultural importance. To facilitate the high-throughput mapping of mutations in Caenorhabditis elegans, we have identified a further 9602

putative new single nucleotide polymorphisms (SNPs) between two  ${\bf C}$ 

. **elegans** strains, Bristol N2 and the Hawaiian mapping strain CB4856, by sequencing inserts from a CB4856 genomic DNA library and using an informatics pipeline to compare sequences with the canonical N2 genomic sequence. When combined with data from other laboratories, our marker set of 17,189 SNPs provides even coverage of the complete worm genome. To date, we have confirmed >1099 evenly spaced SNPs (one every 91 +/- 56 kb) across the six chromosomes and validated the utility of our SNP marker set and new fluorescence polarization-based genotyping methods for systematic and high-throughput identification of genes in  ${\bf C}$ .

elegans by cloning several proprietary genes. We illustrate our approach by recombination mapping and confirmation of the mutation in the cloned gene, dpy-18. [The sequence data described in this paper have been submitted to the NCBI dbSNP data library under accession nos. 4388625-4389689 and GenBank dbSTS under accession nos. 973810-974874. The following individuals and institutions kindly provided reagents, samples, or unpublished information as indicated in the paper: The C. elegans Sequencing Consortium and The

Caenorhabditis Genetics Center.]

L30 ANSWER 2 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:141383 BIOSIS DOCUMENT NUMBER: PREV200200141383

TITLE: The T-box factor MLS-1 acts as a molecular switch during

specification of nonstriated muscle in C.

elegans.

AUTHOR(S): Kostas, Stephen A.; Fire, Andrew (1)

CORPORATE SOURCE: (1) Department of Embryology, Carnegie Institution of

Washington, Baltimore, MD, 21210: fire@ciwemb.edu USA

SOURCE: Genes & Development, (January 15, 2002) Vol. 16, No. 2, pp.

257-269. http://www.genesdev.org/. print.

ISSN: 0890-9369.

DOCUMENT TYPE: Article LANGUAGE: English

AB We have isolated mutations in a gene mls-1 that is required for proper specification of nonstriated muscle fates in Caenorhabditis elegans. Loss of MLS-1 activity causes uterine muscle precursors to forego their normal fates, instead differentiating as vulval muscles. We have cloned mls-1 and shown that the product is a member of the T-box family of transcriptional regulators. MLS-1 acts as a cell fate determinant in that ectopic expression can transform other cell types to

uterine muscle precursors. Uterine muscle patterning is executed by

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           19214 NEMATODE OR C.ELEGANS OR ?ELEGANS
=> S PROLYL?HYDROXYLASE
'?' TRUNCATION SYMBOL NOT VALID WITHIN 'PROLYL?HYDROXYLASE'
The truncation symbol ? may be used only at the end of a search
term. To specify a variable character within a word use '!' 'wom!n' to search for both 'woman' and 'women'. Enter "HELP TRUNCATION" at an arrow prompt (=>) for more information.
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      ANSWER 1 OF 2
                            MEDLINE
ACCESSION NUMBER:
                         2001548313
                                            MEDLINE
DOCUMENT NUMBER:
                         21479120
                                      PubMed ID: 11595184
                         C. elegans EGL-9 and mammalian homologs define a family of dioxygenases that regulate HIF by prolyl hydroxylation. Comment in: Cell. 2001 Oct 5;107(1):1-3
TITLE:
COMMENT:
AUTHOR:
                         Epstein A C; Gleadle J M; McNeill L A; Hewitson K S;
                         O'Rourke J; Mole D R; Mukherji M; Metzen E; Wilson M I;
                         Dhanda A; Tian Y M; Masson N; Hamilton D L; Jaakkola P;
Barstead R; Hodgkin J; Maxwell P H; Pugh C W; Schofield C
                         J; Ratcliffe P J
                         The Henry Wellcome Building of Genomic Medicine, Roosevelt
CORPORATE SOURCE:
                         Drive, Oxford OX3 7BN, United Kingdom. CELL, (2001 Oct 5) 107 (1) 43-54.
SOURCE:
                         Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY:
                         United States
                         Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:
                         English
FILE SEGMENT:
                         Priority Journals
ENTRY MONTH:
                         200112
ENTRY DATE:
                         Entered STN: 20011015
                         Last Updated on STN: 20020420
                         Entered Medline: 20011204
      HIF is a transcriptional complex that plays a central role in mammalian
AR
      oxygen homeostasis. Recent studies have defined posttranslational modification by prolyl hydroxylation as a key regulatory event that
      targets HIF-alpha subunits for proteasomal destruction via the von
      Hippel-Lindau ubiquitylation complex. Here, we define a conserved HIF-VHL-
***prolyl*** ***hydroxylase*** pathway in ***C*** .
         ***elegans***
                             and use a genetic approach to identify EGL-9 as a
      dioxygenase that regulates HIF by prolyl hydroxylation. In mammalian
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series of isoforms bearing a conserved 2-histidine-1-carboxylate iron coordination motif at the catalytic site. Direct modulation of recombinant enzyme activity by graded hypoxia, iron chelation, and cobaltous ions mirrors the characteristics of HIF induction in vivo, fulfilling requirements for these enzymes being oxygen sensors that regulate HIF.

ANSWER 2 OF 2 MEDLINE 79021663 ACCESSION NUMBER: MEDLINE PubMed ID: 212107 79021663 DOCUMENT NUMBER: In vitro translation of nematode cuticular collagens. TITLE: AUTHOR: Noble S; Leushner J; Pasternak J BIOCHIMICA ET BIOPHYSICA ACTA, (1978 Aug 23) 520 (1) SOURCE: 219-28. Journal code: 0217513. ISSN: 0006-3002. PUB. COUNTRY: Netherlands Journal; Article; (JOURNAL ARTICLE) LANGUAGE: English Priority Journals FILE SEGMENT: ENTRY MONTH: 197812 Entered STN: 19900314 **ENTRY DATE:** Last Updated on STN: 19900314 Entered Medline: 19781220 Phenanthroline treatment of growing cultures of the free-living AB\*\*\*nematode\*\*\* Panagrellus silusiae was used to lower the degree of hydroxylation of nascent collagen chains at the polysomal level. Under these conditions, the bound pentasome-hexasome fraction provided substrate for \*\*\*prolyl\*\*\* \*\*\*hydroxylase\*\*\* . When this polysomal fraction was subsequently tested in a cell-free wheat germ system, collagenase-susceptible translation products were observed after sodium dodecyl sulfate-acrylamide gel electrophoresis. The electrophoretic mobilities of each of these four major collagen products were similar to four collagens that are isolated from intact cuticles. In addition, purified polysomal RNA that adhered to unmodified cellulose directed the synthesis of four pepsin-resistant polypeptides that had molecular weights that coincided with four pepsin-resistant collagens that can be purified from the cuticle of this species. Thus, the polysomal site of the messenger RNAs for the cuticular collagens of P. silusiae was located. Although precursor forms of the cuticular collagens were not produced in the cell-free system, the question whether additional amino acid segments occur on the primary translational products of the cuticular collagens in vivo remains open. => D HIS (FILE 'HOME' ENTERED AT 14:44:43 ON 18 JUL 2002) FILE 'MEDLINE' ENTERED AT 14:44:53 ON 18 JUL 2002 19214 S NEMATODE OR C.ELEGANS OR ?ELEGANS L1 L2 509 S PROLYL ?HYDROXYLASE 2 S L1 (S) L2 2 s L1 (L) L2 L4 => S DPY-18 103 DPY 365958 18 L5 DPY-18 (DPY(W)18)=> S DPY-18 OR DPY 103 DPY 365958 18 DPY-18 (DPY(W)18)103 DPY L6 103 DPY-18 OR DPY => S L1 (L) L659 L1 (L) L6 => S L7 AND L2 0 L7 AND L2 L8 => D HIS

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